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Linking terrestrial and aquatic ecosystems: Complexity, persistence and biodiversity in European food webs

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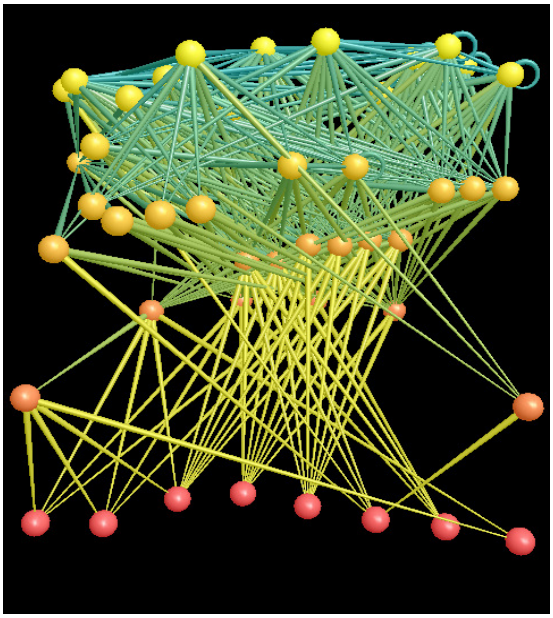

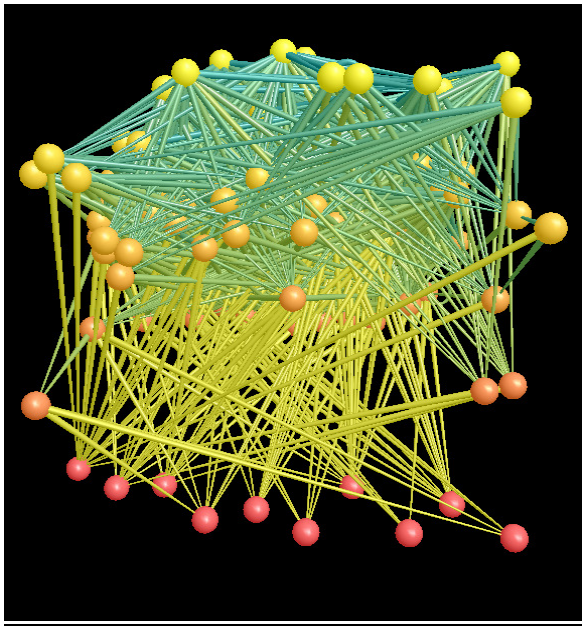

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1. Introduction

The last years have witnessed the emergence of research in the field of complex networks. Complex networks describe a considerable amount of natural and social systems with a large, irregular, and changing in time structure, build up of thousands of nodes and ties between them. Certainly the continuous increase of computational power has supported the analysis of the wide databases of real networks (e.g. among others World Wide Web or social, neural, metabolic networks), and has created the basis for the identification of the unifying laws and statistical properties common to most of these networks (Albert and Barábasi, 2002).

Even though at the beginning it was supposed that complex networks should be treated as random graphs, it was rapidly recognised that this was not always the case and that other types of structures exist, such as small-world (Watts and Strogatz, 1998) and scale free networks (Barabási and Albert, 1999). This is important, since the properties of complex networks are related and/or encoded in their topology. For this reason tools and measurements to capture in quantitative terms these aspects have been developed. Boccaletti et al. (2006) have recently reviewed the indices and structural properties (e.g. size, density, degree, clustering, diameter, etc.) used normally to define network topology, whereas Melián and Bascompte (2004) have shown, for food web networks, how the network structure correlates with its robustness and its response to external perturbations, showing that the cohesive organization of a network in dense sub webs increases the resistance against fragmentation.

A food web constitutes a special description of a biological community with focus on trophic interactions between consumers and resources (de Ruiter et al., 2005). Therefore, food webs are deeply interrelated with ecosystem processes and functioning since the trophic interactions represent the transfer rates of energy and matter within the ecosystem. In addition, the study of ecological network structure and stability provides an important tool in the assessment of the impact of perturbations in the ecosystem itself. In particular it is known that trophic webs are not randomly assembled, but are the result of the interaction of different cohesive subgroups. Therefore, identifying the tightly connected groups within a network is an important tool for understanding the main energy flows of the network itself, as well as for defining a hierarchy of nodes and connections within a complex structure (Boccaletti et al., 2006). For this reason a considerable effort in ecosystems theory has been devoted to understand how food webs are structured and how this structure influence ecosystem processes.

In addition the introduction of dynamics, through bionergetic-based models, in food webs has allowed the development of explicit dynamic network models of shared nutrient consumption,

including competition among produces for multiple resources, as well as effects of anthropogenic pressures. This has also allowed to include population dynamics within this framework (Martinez et al., 2006) and to extend the type of network parameters and analysis one is able to calculate.

However, despite the ubiquity of complex ecosystems and the vast numbers of interaction between different species, a higher food web complexity has been demonstrated not correlated with a higher stability (May, 1972, 1974). In recent studies on adaptive networks (Garcia-Domingo, Saldana, in press), different configurations of trophic networks and nonlinear bioenergetic dynamics (Dunne et al., 2004; Martinez et al., 2005; Boccaletti et al., 2006) are helping to elucidate the relation between ecological stability and complexity in food webs. In particular, it has been observed that little cohesive groups of nodes in the food webs represent groups of key species that make the entire network more resistant to external perturbation, decreasing the probability of network fragmentation when species are removed (Melián and Bascompte, 2004). Several definitions of cohesive sub groups or clusters have been proposed to analyse this effect (de Nooy et al., 2005), such as K-cores, cliques, components.

Our purpose is to define terrestrial and aquatic food web networks at selected European sites prototypical of European ecosystems and then analyze the network structure, properties and composition of cohesive sub webs. The analysis will focus in particular on the link between terrestrial and aquatic ecosystem. In a second step, we plan to add the spatio-temporal dynamics in those food webs and then to examine their changing properties. Finally, we would like to assess the network persistence when subjected to anthropogenic pressures linked to the application of several environmental EU policies.

In this work, we present the preliminary results for two food webs and develop the general strategy. It is clear that, in order to carry out a comparative analysis, we need to extend the spatial coverage including at least one representative site for each European ecosystem. Our work is continuing across these lines.

2. Materials and Methods

2.1. Habitat type classification

EUNIS Habitat type classification (http://eunis.eea.europa.eu/) is a comprehensive pan-European system to facilitate the harmonised description and collection of data across Europe through the use of criteria for habitat identification. It covers all types of habitats from natural to artificial, from terrestrial to freshwater and marine (see Fig. 1 as an example).

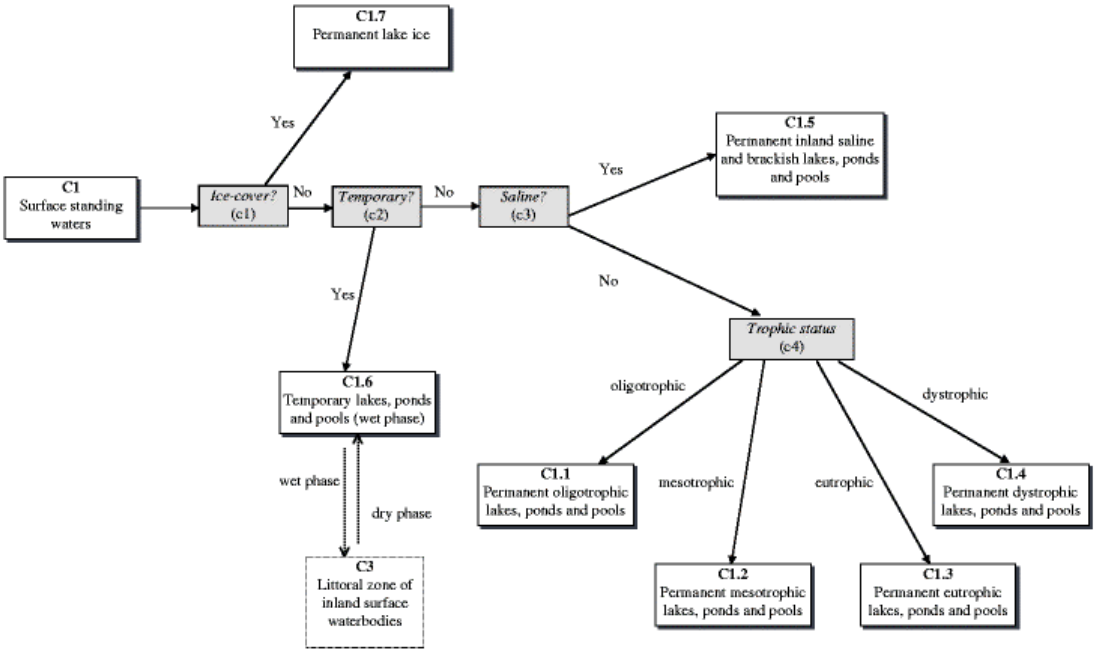

Figure 1. EUNIS habitat classification criteria for surface standing waters (http://eunis.eea.europa.eu/).

In this work, habitat type is defined, taking into account the EUNIS habitat type classification, as follows: 'Plant and animal communities as the characterizing elements of the biotic environment, together with abiotic factors operating together at a particular scale.'

Food webs have been analysed and defined for several surface standing waters European sites including lakes, ponds and pools of natural origin containing fresh (i.e. nonsaline), brackish or salt water, manmade freshwater bodies, including artificially created lakes, reservoirs and canals (Fig. 1). These sites have been divided in saline (littoral and inland) and freshwater habitat, while habitats with permanent snow and ice have been excluded. A sub-classification in reference to trophic status has been applied (oligotrophic, mesotrophic, eutrophic and dystrophic). Terrestrial vegetation and fauna have been considered in the development of trophic webs. The sites belonging to different macroscopic biogeographic European regions can be seen in Table 1.

Table 1. List of standing water sites in Europe grouped by country and biogeographical region (http://eunis.eea.europa.eu/).

Biogeographic region	Country	Standing water sites
Alpine	Bulgaria	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 6 sites
	Finland	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 1 site
	Former Yugoslav Rep. of Macedonia	via CORINE Biotopes 22 (Standing fresh water), 3 sites
	France	via CORINE Biotopes 22 (Standing fresh water), 20 sites; 22.1 (Permanent ponds and lakes), 11 sites; 22.42 (Rooted submerged vegetation), 2 sites
	Germany, Federal Republic of	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 7 sites; 22.44 (Chandalier algae submerged carpets), 2 sites; 22.45 (Peatmoss-bladderwort bog pools), 2 sites
	Italy	via CORINE Biotopes 22 (Standing fresh water), 100 sites
	Poland	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 8 sites; 22.42 (Rooted submerged vegetation), 3 sites
	Romania	via CORINE Biotopes 22 (Standing fresh water), 2 sites; 22.1 (Permanent ponds and lakes), 12 sites; 22.42 (Rooted submerged vegetation), 1 site
	Slovenia	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 3 sites; 22.42 (Rooted submerged vegetation), 2 sites
	Slovakia	via CORINE Biotopes 22.41 (Free-floating vegetation), 2 sites; 22.43 (Rooted floating vegetation), 1 site
Atlantic	Belgium	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.1 (Permanent ponds and lakes), 1 site; 22.41 (Free-floating vegetation), 6 sites; 22.42 (Rooted submerged vegetation), 9 sites; 22.43 (Rooted floating vegetation), 4 sites; 22.44 (Chandalier algae submerged carpets), 1 site
	Denmark	via CORINE Biotopes 22 (Standing fresh water), 10 sites; 22.44 (Chandalier algae submerged carpets), 1 site
	France	via CORINE Biotopes 22 (Standing fresh water), 30 sites; 22.1 (Permanent ponds and lakes), 21 sites; 22.41 (Free-floating vegetation), 30 sites; 22.42 (Rooted submerged vegetation), 46 sites; 22.43 (Rooted floating vegetation), 12 sites; 22.44 (Chandalier algae submerged carpets), 5 sites
	Germany, Federal Republic of	via CORINE Biotopes 22 (Standing fresh water), 4 sites; 22.1 (Permanent ponds and lakes), 98 sites; 22.41 (Free-floating vegetation), 29 sites; 22.42 (Rooted submerged vegetation), 33 sites; 22.43 (Rooted floating vegetation), 21 sites; 22.45 (Peatmoss-bladderwort bog pools), 1 site
	Ireland	via CORINE Biotopes 22 (Standing fresh water), 35 sites; 22.1 (Permanent ponds and lakes), 40 sites; 22.41 (Free-floating vegetation), 8 sites; 22.42 (Rooted submerged vegetation), 52 sites; 22.43 (Rooted floating vegetation), 45 sites; 22.44 (Chandalier algae submerged carpets), 33 sites
	Netherlands	via CORINE Biotopes 22 (Standing fresh water), 2 sites; 22.1 (Permanent ponds and lakes), 25 sites; 22.41 (Free-floating vegetation), 2 sites; 22.42 (Rooted submerged vegetation), 2 sites; 22.43 (Rooted floating vegetation), 4 sites; 22.44 (Chandalier algae submerged carpets), 12 sites
	Portugal	via CORINE Biotopes 22 (Standing fresh water), 1 site
	Spain	via CORINE Biotopes 22.41 (Free-floating vegetation), 4 sites
	United Kingdom	via CORINE Biotopes 22 (Standing fresh water), 81 sites; 22.41 (Free-floating vegetation), 2 sites; 22.42 (Rooted submerged vegetation), 2 sites; 22.43 (Rooted floating vegetation), 1 site
Black Sea	Bulgaria	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 1 site
	Romania	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.1 (Permanent ponds and lakes), 8 sites
Boreal	Estonia	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 4 sites; 22.41 (Free-floating vegetation), 3 sites; 22.42 (Rooted submerged vegetation), 3 sites; 22.43 (Rooted floating vegetation), 3 sites
	Finland	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.1 (Permanent ponds and lakes), 24 sites; 22.42 (Rooted submerged vegetation), 1 site; 22.43 (Rooted floating vegetation), 5 sites; 22.44 (Chandalier algae submerged carpets), 1 site
	Latvia	via CORINE Biotopes 22 (Standing fresh water), 82 sites; 22.1 (Permanent ponds and lakes), 2 sites; 22.42 (Rooted submerged vegetation), 7 sites; 22.44 (Chandalier algae submerged carpets), 3 sites
	Lithuania	via CORINE Biotopes 22 (Standing fresh water), 8 sites; 22.1 (Permanent ponds and lakes), 108 sites; 22.41 (Free-floating vegetation), 30 sites; 22.42 (Rooted submerged vegetation), 23 sites; 22.43 (Rooted floating vegetation), 28 sites; 22.44 (Chandalier algae submerged carpets), 9 sites; 22.45 (Peatmoss-bladderwort bog pools), 7 sites
Continental	Belgium	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 1 site; 22.41 (Free-floating vegetation), 20 sites; 22.42 (Rooted submerged vegetation), 23 sites; 22.43 (Rooted floating vegetation), 16 sites; 22.44 (Chandalier algae submerged carpets), 1 site
	Bulgaria	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 7 sites
	Czech Republic	via CORINE Biotopes 22 (Standing fresh water), 8 sites; 22.1 (Permanent ponds and lakes), 18 sites; 22.41 (Free-floating vegetation), 6 sites; 22.42 (Rooted submerged vegetation), 6 sites; 22.43 (Rooted floating vegetation), 14 sites; 22.45 (Peatmoss-bladderwort bog pools), 3 sites

	Denmark	via CORINE Biotopes 22 (Standing fresh water), 11 sites
	Former Yugoslav Rep. of Macedonia	via CORINE Biotopes 22 (Standing fresh water), 1 site
	France	via CORINE Biotopes 22 (Standing fresh water), 33 sites; 22.1 (Permanent ponds and lakes), 21 sites; 22.41 (Free-floating vegetation), 11 sites; 22.42 (Rooted submerged vegetation), 23 sites; 22.43 (Rooted floating vegetation), 13 sites; 22.44 (Chandalier algae submerged carpets), 4 sites
	Germany, Federal Republic of	via CORINE Biotopes 22 (Standing fresh water), 63 sites; 22.1 (Permanent ponds and lakes), 424 sites; 22.41 (Free-floating vegetation), 102 sites; 22.42 (Rooted submerged vegetation), 114 sites; 22.43 (Rooted floating vegetation), 102 sites; 22.44 (Chandalier algae submerged carpets), 30 sites; 22.45 (Peatmoss-bladderwort bog pools), 33 sites
	Italy	via CORINE Biotopes 22 (Standing fresh water), 74 sites
	Lithuania	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 1 site
	Luxembourg	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 4 sites; 22.41 (Free-floating vegetation), 1 site; 22.42 (Rooted submerged vegetation), 1 site; 22.43 (Rooted floating vegetation), 1 site
	Poland	via CORINE Biotopes 22 (Standing fresh water), 37 sites; 22.1 (Permanent ponds and lakes), 235 sites; 22.41 (Free-floating vegetation), 37 sites; 22.42 (Rooted submerged vegetation), 11 sites; 22.43 (Rooted floating vegetation), 5 sites; 22.44 (Chandalier algae submerged carpets), 3 sites; 22.45 (Peatmoss-bladderwort bog pools), 21 sites
	Romania	via CORINE Biotopes 22 (Standing fresh water), 2 sites; 22.1 (Permanent ponds and lakes), 13 sites; 22.41 (Free-floating vegetation), 1 site
	Slovenia	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.41 (Free-floating vegetation), 4 sites; 22.42 (Rooted submerged vegetation), 2 sites; 22.43 (Rooted floating vegetation), 2 sites
Macaronesian	Portugal	via CORINE Biotopes 22 (Standing fresh water), 2 sites; 22.1 (Permanent ponds and lakes), 11 sites; 22.42 (Rooted submerged vegetation), 1 site
Mediterranean	Albania	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.41 (Free-floating vegetation), 1 site; 22.42 (Rooted submerged vegetation), 1 site
	Former Yugoslav Rep. of Macedonia	via CORINE Biotopes 22 (Standing fresh water), 1 site; 22.1 (Permanent ponds and lakes), 1 site
	France	via CORINE Biotopes 22 (Standing fresh water), 9 sites; 22.1 (Permanent ponds and lakes), 4 sites; 22.42 (Rooted submerged vegetation), 5 sites; 22.43 (Rooted floating vegetation), 1 site; 22.44 (Chandalier algae submerged carpets), 1 site
	Greece	via CORINE Biotopes 22 (Standing fresh water), 59 sites; 22.1 (Permanent ponds and lakes), 4 sites
	Italy	via CORINE Biotopes 22 (Standing fresh water), 164 sites
	Portugal	via CORINE Biotopes 22 (Standing fresh water), 25 sites; 22.1 (Permanent ponds and lakes), 6 sites; 22.41 (Free-floating vegetation), 1 site; 22.42 (Rooted submerged vegetation), 1 site; 22.43 (Rooted floating vegetation), 2 sites
	Spain	via CORINE Biotopes 22.41 (Free-floating vegetation), 19 sites; 22.42 (Rooted submerged vegetation), 6 sites; 22.43 (Rooted floating vegetation), 2 sites; 22.44 (Chandalier algae submerged carpets), 3 sites; 22.45 (Peatmoss-bladderwort bog pools), 1 site
Pannonian	Czech Republic	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 3 sites; 22.41 (Free-floating vegetation), 4 sites; 22.42 (Rooted submerged vegetation), 1 site; 22.43 (Rooted floating vegetation), 2 sites
	Hungary	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 9 sites; 22.41 (Free-floating vegetation), 7 sites; 22.42 (Rooted submerged vegetation), 7 sites; 22.43 (Rooted floating vegetation), 6 sites; 22.44 (Chandalier algae submerged carpets), 2 sites
	Slovakia	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 1 site; 22.41 (Free-floating vegetation), 5 sites; 22.43 (Rooted floating vegetation), 3 sites
	Romania	via CORINE Biotopes 22.1 (Permanent ponds and lakes), 2 sites; 22.43 (Rooted floating vegetation), 1 site
Steppic	Romania	via CORINE Biotopes 22 (Standing fresh water), 2 sites; 22.1 (Permanent ponds and lakes), 7 sites

2.2. Data collection and food items information

The main challenge in the modelling of real trophic networks is data collection. In order to develop a coherent food web structure, data on species composition from consolidated database and data on diet of each species are needed. However, the availability of these data sets is scarce and development is needed if EU biodiversity is to be preserved. Additional effort is needed.

Due to the presence of thousand of species in real ecosystems, commonly species with similar ecological behaviour and diet composition are pooled in the same ecological compartment.

A list of used database and references is available in each summary table relative of trophic networks analyzed (Tables. 2-3).

A relevant part of information on species composition of European food webs is available at the EUNIS Database web application (http://eunis.eea.europa.eu). The database includes the access to publicly available data on species, habitats and sites compiled in the framework of NATURA2000 (EU Habitats and Birds Directives) and EMERALD (Network of the Bern Convention); data collected from frameworks, data sources or material published by ETC/BD (formerly the European Topic Centre for Nature Conservation); information on species, habitats and sites taken into account in relevant international conventions or from International Red Lists and data collected in the framework of the EEA's reporting activities.

In particular we used information contained in CORINE biotopes database, details on CORINE experimental work programme of the Commission of the European Communities, are available at http://reports.eea.europa.eu/COR0-biotopes-index/en.

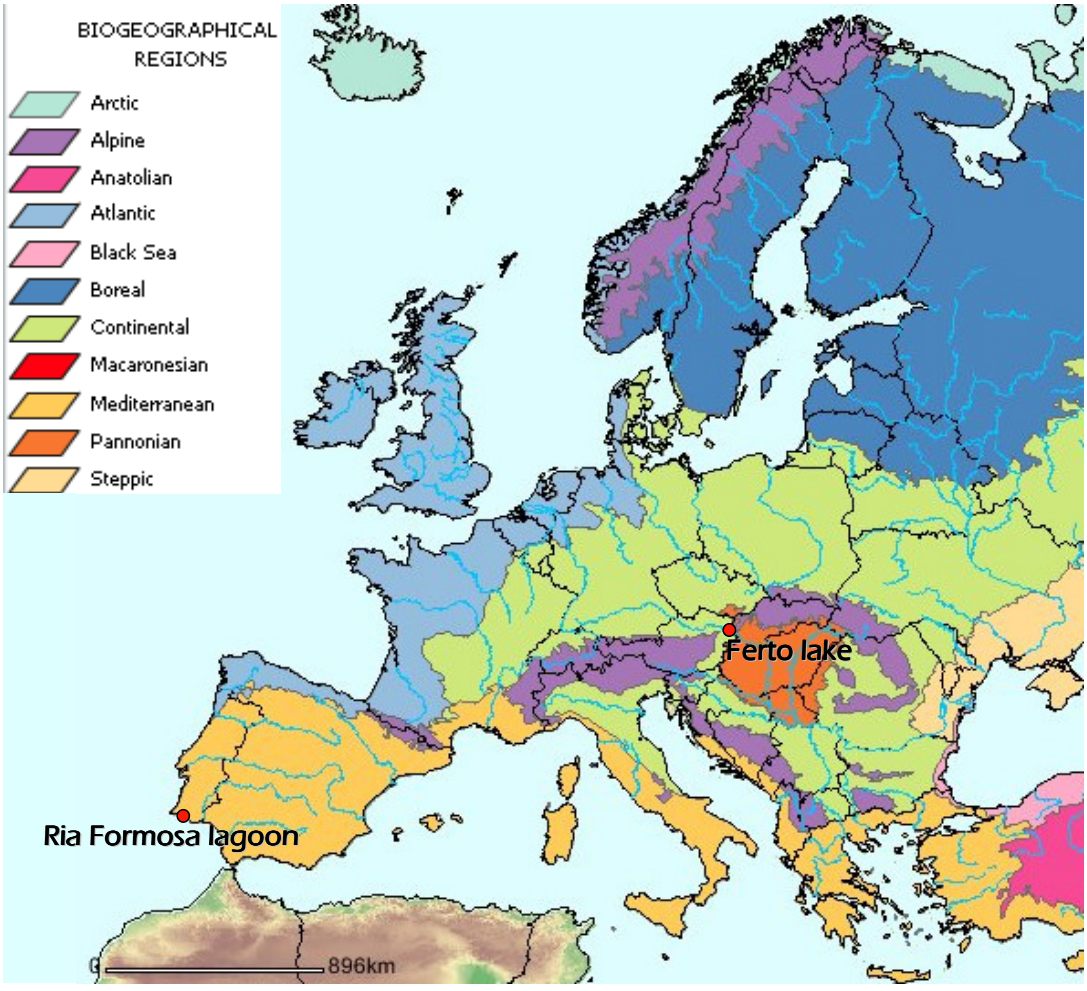

Figure 2. Map of European biogeographical regions (http://eunis.eea.europa.eu). Sites selected for defining typical food webs are pointed out.

2.3. Food web analysis

Network proprieties like diversity, connectivity, clustering etc. have been analysed with a freely available not-commercial use program Pajek (http://vlado.fmf.uni-lj.si/pub/networks/pajek/).

Pajek (spider in Slovenian) is a program developed for the analysis and visualization of large networks. It was developed to help in the decomposition of large networks into more tractable and smaller networks; to provide visualization tools and to provide efficient algorithms for network analysis (de Nooy et al., 2005).

2.4. Food web dynamics

Persistence and stability of trophic webs can be predicted and investigated with an integrated modelling approach of ecosystem structure and dynamics as proposed by Martinez and Williams (2001 Santa Fe Institute Working Paper 01-07-037); the freely available-not commercial software FoodWeb3D (Wiliams, 2003) has been used to analyze the integrated terrestrial and aquatic food webs of selected European sites.

2.5. Measures of network cohesion and persistence

Food web networks normally contain several sub groups with a major number of interactions, in general terms the number of ties is directly correlated to cohesion of the net. Several techniques exist to detect the cohesive subwebs and in particular the following indices have been calculated for each network and sub network: density, degree, weak components, strong components, k-cores and cliques (de Nooy et al., 2005).

The density of a network (in several paper density is called connectance) is calculated as percentage of ties that are present in relation to all possible ties in the network: $C=L/S^2$ where L are number of links in the network and S are number of vertices. In empirical food webs density has a range between 0.03 and 0.3, with a central tendency between 0.1 and 0.15 (Pascual and Dunne, 2006; Dunne et al., 2002). Ties can have a direction; in this case we have arcs. Normally, the value of density is inversely correlated to the size of the network, and therefore it is difficult compare networks with different number of nodes. For this reason it is better to use other indices such as: the degree of a vertex, that represent the number of lines incident with one node (or vertex) and the mean degree of all nodes as a measure of overall cohesion of the network. It is possible to calculate also the outdegree and the indegree, taking into account respectively only number of incoming or outgoing lines.

A weak component in a network is a maximal weakly connected subweb: in this case vertices of the subnetwork are connected so that is possible to travel from a vertex to another and

return at the starting point, no vertex between the first and the last vertex in the component occurs more than once and the direction of arcs is not considered.

A strong component is a maximal strongly connected subweb: the definition is the same as previously, but in this case the direction of the arcs is taken into account.

A k-core is defined as a maximal subnetwork in which each vertex has at least degree k within the subweb. Incoming or outgoing lines can be considered separately or together. Cores with higher ranking values indicate densest zones of the considered network. K cores can be split in several strong components.

Clique is a stricter definition of subweb and indicates a set of vertices in which each vertex is directly connected to all other vertices. In general clique with a minimum of three vertices are considered (triads).

Persistence of the network has been calculated as the ratio between species at the beginning and at the end of a non linear dynamical simulation performed in the freely available bioenergetic model FoodWeb3D (Wiliams, 2003), as proposed by Martinez et al. (2005).

In the dynamic model the variation of biomass *B* of a species *i* in a trophic network over the time *t* it is calculated as:

$$B_i^{'} = G_i \cdot (B) - x_i \cdot B_i \cdot (t) + \sum_{j=1}^{n} \left(\frac{x_i y_{ij} \alpha_{ij} F_{ij}(B) B_i(t) - x_j y_{ji} \alpha_{ji} F_{ji}(B) B_{ji}(t)}{e_{ji}} \right)$$

Where the first term refers to the gross primary production rate of species *i*, the second term is the metabolic loss and the third term represents gains from preys and losses toward predators.

The rate x_i is the mass specific metabolic rate of species *i*; y_{ij} is the maximum assimilation efficiency rate of species *i* (predator) on species *j* (prey); α_{ij} indicate the relative fraction of prey *j* in the diet of consumer *i*, and is assigned on a basis of topology of the network so that the summation of α_{ij} for consumer species is 1 and for primary producers is 0. The functional response $F_{ij}(B)$ is a function of the prey biomass and indicates the maximum ingestion rate of predator *i* consuming a prey *j*. The parameter e_{ij} is the conversion efficiency of the biomass lost by prey in biomass assimilated by the consumers (Martinez et al., 2005).

2.6. Measures of biodiversity

Biodiversity in each site has been measured by means of two well known indices: Shannon Wiener and Simpson's indices. The Shannon-Weiner index (H') is calculated as:

$$H^{'} = -\sum p_i \ln p_i$$

where p_i is he proportional abundance of species i in the sample. This index can vary between 0 and ∞.

The Simpson's index (D) measures the probability that two individuals randomly selected from a sample will belong to the same species, has values between 0 and 1 and is given by:

$$D = \sum p_i^{\,2}$$

The Shannon index is more sensible to rare species, due to the presence of the logarithmic function.

Unfortunately, there is not enough information in the two case studies analysed to estimate the relative abundance of each species, therefore we have considered only the number of species belonging to each ecological compartment and we have applied the indices at the compartment level.

3. Case studies

Since our purpose is to develop a general strategy for analysing European terrestrial and aquatic ecosystems under anthropogenic pressures and assessing the role of EU environmental policies, we present here only two case studies to illustrate the approach. Further development in terms of spatial coverage and types of ecosystems is needed in order to be able to perform intercomparative analysis.

3.1. Lake Ferto trophic network

3.1.1. Specific site information

Lake Ferto /Neusiedler See (latitude: 47°37′–47°57′, longitude 16°41′–16°52′), with a surface area of 309 Km^2, mean depth of 1.1 m and maximum depth 1.3 m, is the westernmost and largest steppe lake in Eurasia. It is located in Hungary and is covered for 54 % of its surface by reed (Phragmites australis) (Dinka et al., 2004). Ferto lake was declared as a biosphere reserve by UNESCO in 1977 and 1979 put on the World Heritage list.

The extreme shallowness of the lake lead to a formation of large reed colonized areas also in the inner zone, and the induced fragmentation sustain the important habitat diversity (Dinka et al., 2004).

This lake can be described as a shallow, saline (conductivity of 1.3–3.5 mS cm^{-1} and pH of 7.7–9.5) (Agoston-Szabo et al., 2006), turbid, mesotrophic lake. Two small permanent tributaries (Rácos and Wulka streams) and an underground affluent represent the water input of the lake (Reitinger, 1990).The lake is surrounded by humid grasslands and saline meadows, where avifauna finds shelter and rest areas. The surrounding landscape is a patchwork of forest, pastureland and a network of drainage canals, in particular zones with short grass are essential for the survivor of small mammals, favourite prey of *falconidae* families (Haberl, and Krysťufek, 2003).

Trophic network compartments considered and information about species composition and diet are summarized in Table 2.

Table. 2. Summary of compartments, species or group of species and nodes in the lake Ferto web; databases and references relative to species composition and diet are reported.

Reference species composition	Compartments	Species or groups	Nodes	References diet
Paulovits and Biro, 1986; CORINE	Fish	12	12	http://www.fishbase.org/ (Jellyman,1989)
CORINE	Amphibians	3	3	http://amphibiaweb.org/index.html
CORINE	Mammals	3	3	http://www.abdn.ac.uk/mammal/index.shtml; http://animaldiversity.ummz.umich.edu/site/index.html; Batzli and Lesieutre,1991; Tast, 1966;Wilson and Ruff. 1999
CORINE	Reptiles	3	3	http://animals.jrank.org/; http://www.arkive.org/
CORINE	Birds	10	10	http://www.hawk-conservancy.org; http://www.specolalive.it; http://www.oiseaux.net/oiseaux; http://aves.ccg.pt/; http://www.birdlife.org; Jaensch, 2006;Tsachalidis & Goutner, 2002;http://algol.sirius.pisa.it/lipupisa/tarabuso.htm; Antczaket al., 2002
Ildikó Varga, 2003	Macroinvertebrates	40	4	Ildikó Varga, 2003
Kiss, 2002	Meso-Macrozooplankton	3	1	Riedl, 1991
	Micro zooplankton	1	1	Riedl, 1991
Borsodi et al., 1998; Agoston-Szabo et al., 2006	Bacteria	7	1	
Agoston-Szabo et al., 2006	Fungi	1	1	
	Phytoplankton	1	1	
	Benthic Algae	1	1	
	Epiphites	1	1	
CORINE; Agoston-Szabo et al., 2006	Plants	22	1	
	Benthic detritus	1	1	
	Plankton detritus	1	1	

3.1.2. Network analysis

A representation of lake Ferto food web is shown in Fig. 3, where names of species or group of species are shown and colours indicate different trophic compartment; primary producers and detritus are on the top and predators on the bottom. The total number of vertices is 45, connected by 350 ties and 7 loops, the total density of the network is 0.1728, and therefore 17% of possible arcs are present in the network.

In Table 3 number of vertices in each class of degree is listed: in the first column (class) numbers of connections are indicated, the second column contains number of vertices belonging to each class, the third column the frequency per cent, and the two last columns cumulative frequency and cumulative frequency per cent (e.g. one vertex, having 2 connection, belong to the first class, which is 2.2 percent of all compartments).

Frequency of vertex with degree from 2 to 30 have been detected inside the network, the frequency distribution of degree appear homogeneous. Macroinveterbrates, as connection ring between primary producers and higher trophic levels, are classes with higher degree, followed by generalist omnivorous predators.

Mean degree of the network is 15.55 (standard deviation 8.08) and if we normalize the network, dividing by the number of potential neighbours, mean normalized degree is 0.17 (standard deviation 0.09).

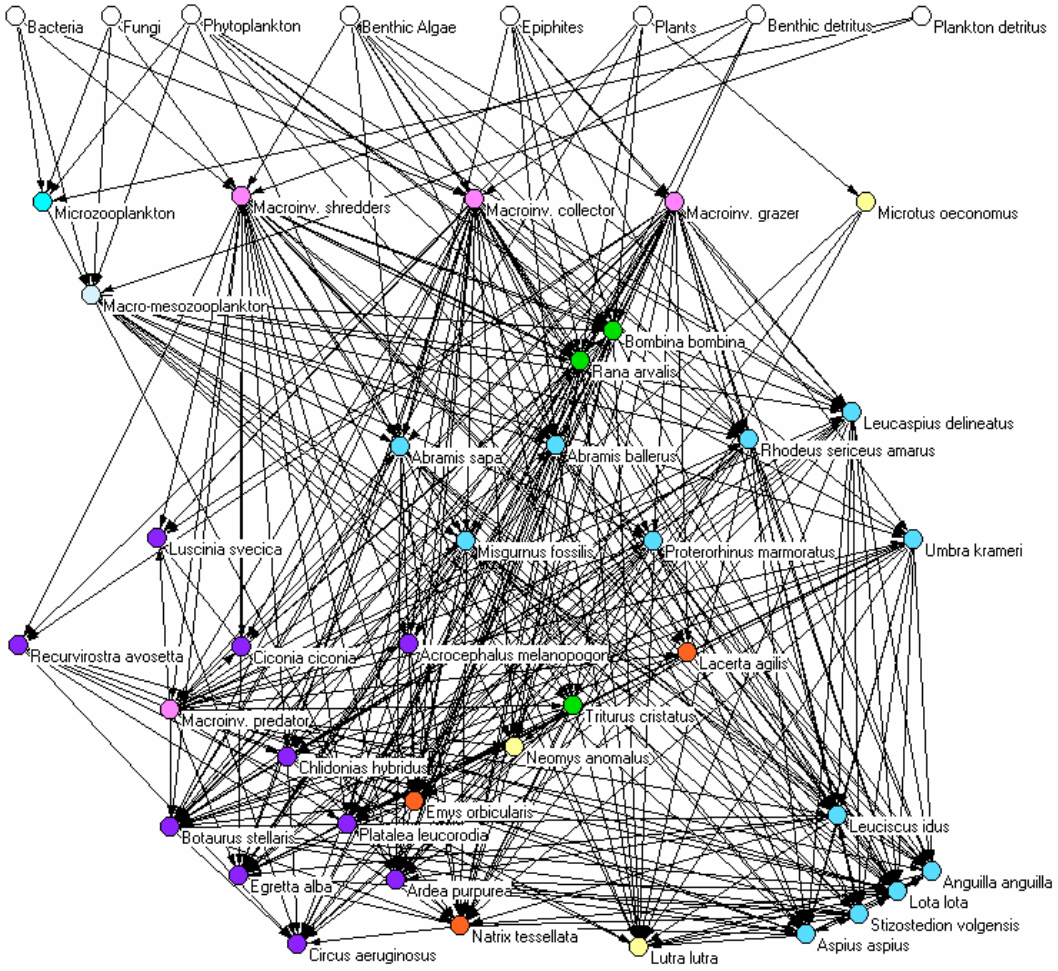

Figure 3. Lake Ferto trophic network, species are ordered according to their trophic level, colours indicate different compartments.

Table 3. Frequency distribution of degree in the lake Ferto net.

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
2	1	2.2222	1	2.2222	Plankton detritus
4	5	11.1111	6	13.3333	Ciconia ciconia
5	2	4.4444	8	17.7778	Microzooplankton
6	1	2.2222	9	20.0000	Acrocephalus melanopogon
7	2	4.4444	11	24.4444	Luscinia svecica
8	2	4.4444	13	28.8889	Lacerta agilis
9	2	4.4444	15	33.3333	Recurvirostra avosetta
11	1	2.2222	16	35.5556	Neomys anomalus
13	2	4.4444	18	40.0000	Chlidonias hybridus
15	1	2.2222	19	42.2222	Platalea leucorodia
16	1	2.2222	20	44.4444	Triturus cristatus
17	2	4.4444	22	48.8889	Lutra lutra
18	3	6.6667	25	55.5556	Ardea purpurea
19	4	8.8889	29	64.4444	Egretta alba
20	4	8.8889	33	73.3333	Macro-mesozooplankton
21	3	6.6667	36	80.0000	Rhodeus sericeus amarus
22	1	2.2222	37	82.2222	Stizostedion volgensis
23	1	2.2222	38	84.4444	Leuciscus idus
25	1	2.2222	39	86.6667	Natrix tessellata
26	1	2.2222	40	88.8889	Botaurus stellaris
27	2	4.4444	42	93.3333	Macroinv. grazer
29	1	2.2222	43	95.5556	Macroinv. predator
30	2	4.4444	45	100.0000	Macroinv. shredders

The input and output k core partition take into account degree of vertices, considering respectively incoming and outgoing lines: three cores are detected in both cases (figure 4). The position of vertices in the cores is, in general, in agreement with the trophic levels: higher scores for input k cores belong to top predatos and for output cores to primary producers, with the exception, in output cores, of top fish predators that are caught mainly by birds and to a less extent by mammals.

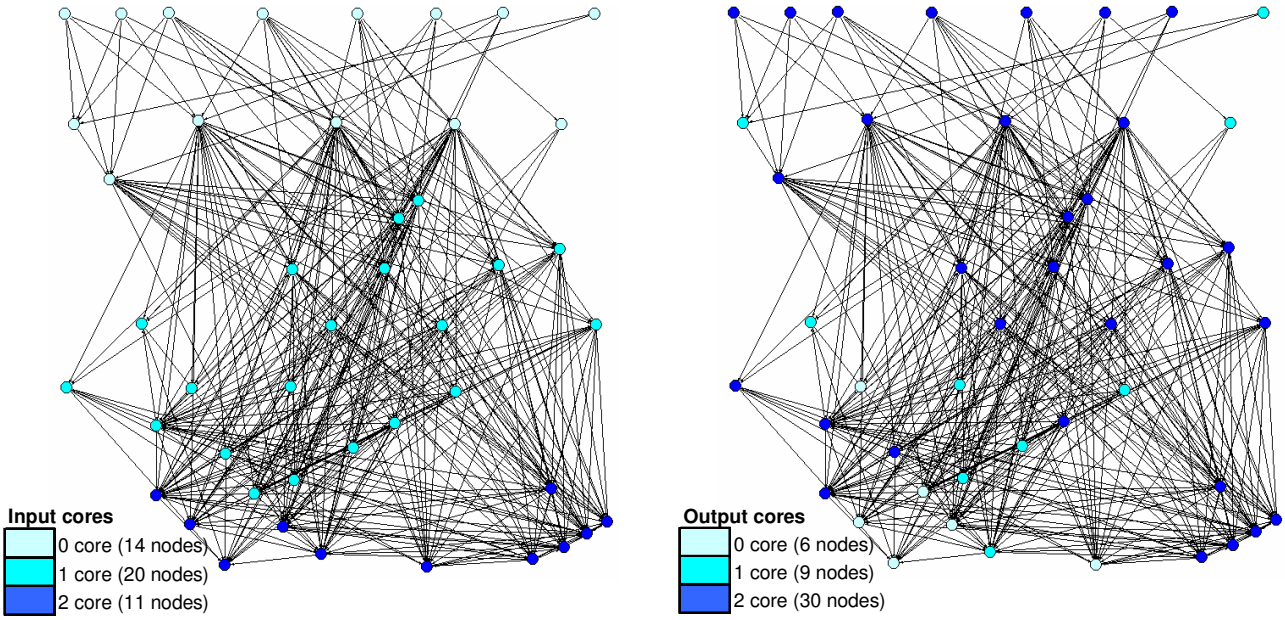

Figure 4. Input and output cores in the Ferto lake network, colours indicate vertices belonging the different cores.

In the k core partition (not considering direction of ties) (Fig 5 and Table 4) one big densest sub web with a corresponding density of 13 links for each vertex within the core has been detected; two other subwebs with low density are present. The distribution of k cores follows with a good approximation a logarithmic law (Fig. 6). The densest sub web contains all fish, macroinvetebrates, amphibians compartments, some birds and reptiles and the mammal *Lutra lutra*, whereas main primary producers and detritus classes belong to a cohesive sub group with lower density (4 links for vertex). Only one strong component, mainly composed by fish species (Fig. 7), has been detected inside the densest subweb. Eliminations of cores with lower values do not split the network into separate components. Many weak components and weak triads (Table 5) are present inside the Ferto net. Triads overlap on the great part on macroinvertebrates compartments, as shown in Table 5.

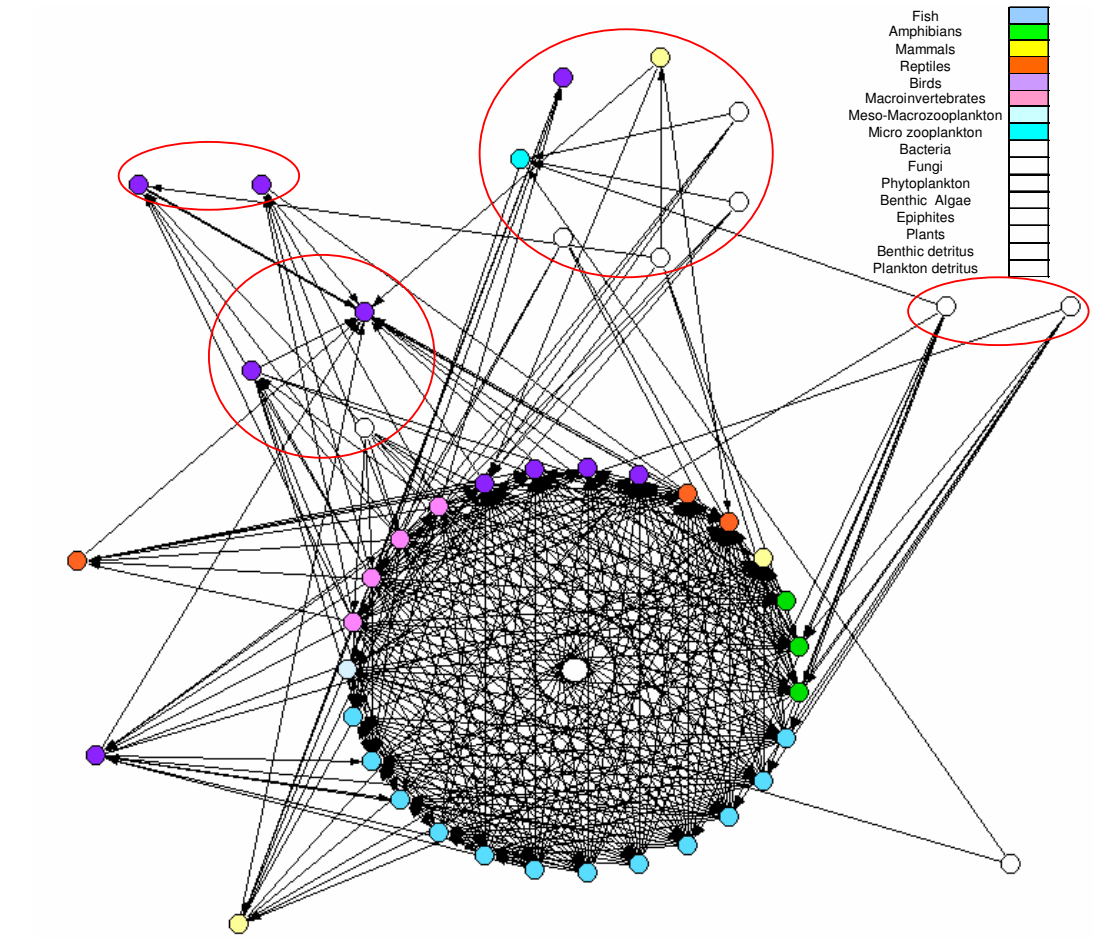

Figure 5. K-cores partition in lake Ferto network, colours indicate different compartment. Red circles indicate the smaller cores.

Table 4. Frequency distribution of k-cores in the lake Ferto network.

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
2	1	2.2222	1	2.2222	Plankton detritus
4	7	15.5556	8	17.7778	Microzooplankton
6	2	4.4444	10	22.2222	Luscinia svecica
7	2	4.4444	12	26.6667	Phytoplankton
8	1	2.2222	13	28.8889	Lacerta agilis
9	3	6.6667	16	35.5556	Recurvirostra avosetta
10	1	2.2222	17	37.7778	Neomys anomalus
12	1	2.2222	18	40.0000	Chlidonias hybridus
13	27	60.0000	45	100.0000	Macro-mesozooplankton

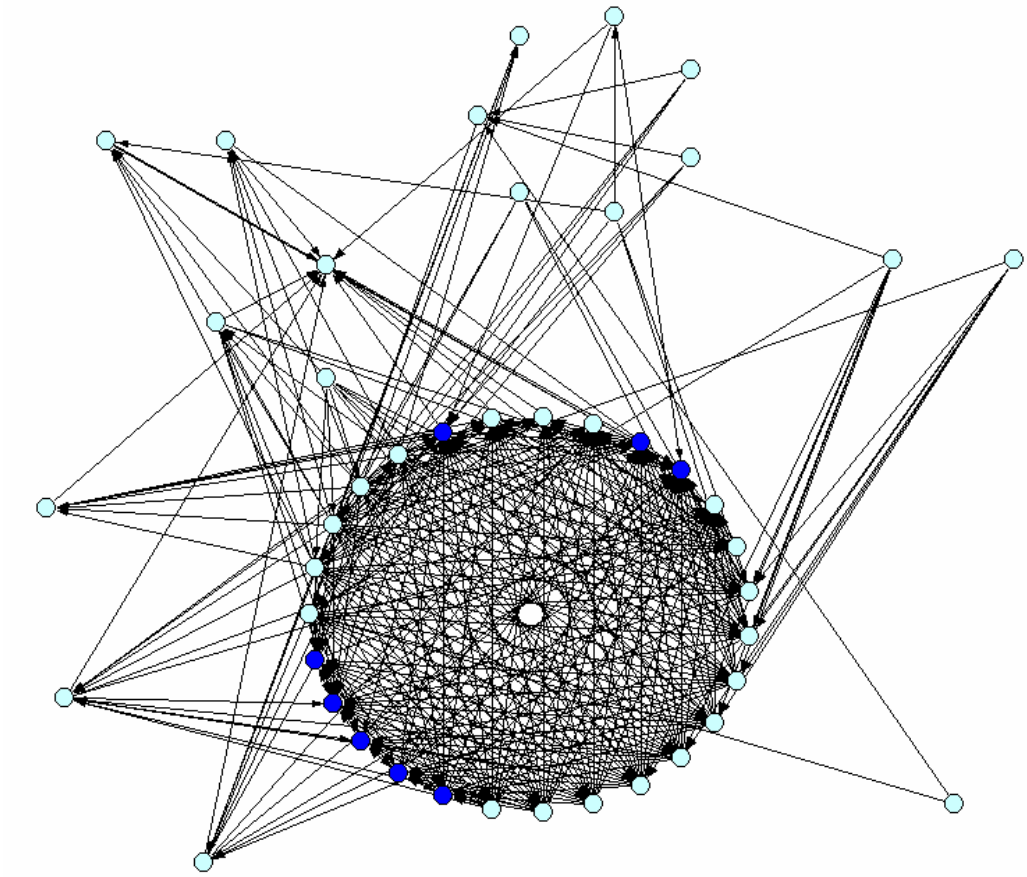

Figure 6. K-cores partition in lake Ferto network, colour blue indicates a strong component.

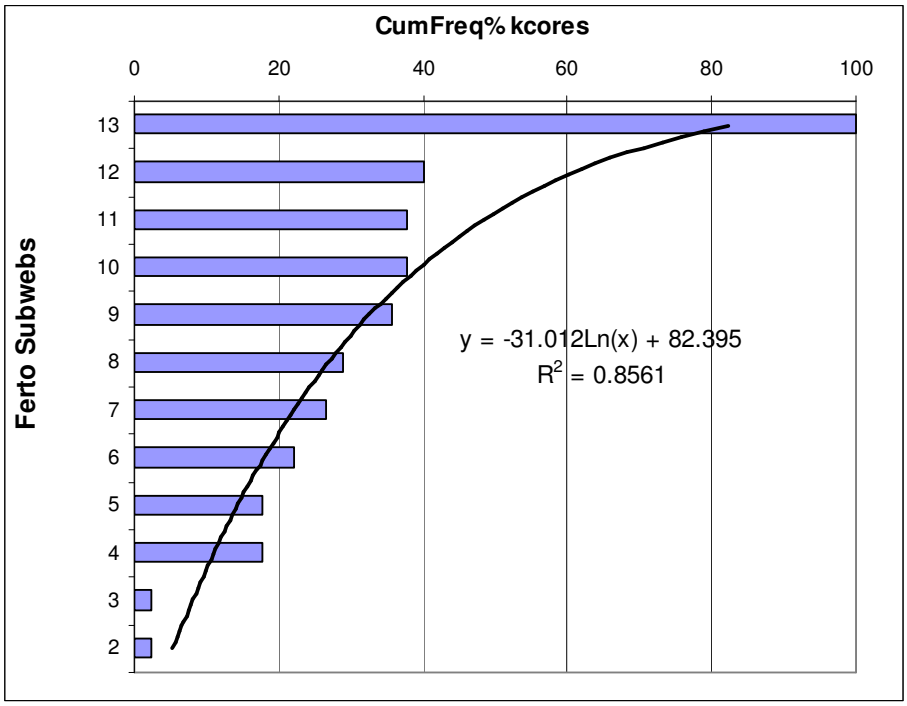

Figure 7. K-subwebs cumulative frequency distribution in Ferto net.

Table 5. Frequency distribution of triads in the lake Ferto network.

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
6	3	6.6667	3	6.6667	38
18	2	4.4444	5	11.1111	11
24	5	11.1111	10	22.2222	1
36	1	2.2222	11	24.4444	42
42	1	2.2222	12	26.6667	40
78	1	2.2222	13	28.8889	9
96	1	2.2222	14	31.1111	18
108	1	2.2222	15	33.3333	41
138	1	2.2222	16	35.5556	16
216	1	2.2222	17	37.7778	21
234	1	2.2222	18	40.0000	23
270	1	2.2222	19	42.2222	12
330	1	2.2222	20	44.4444	22
336	2	4.4444	22	48.8889	24
354	2	4.4444	24	53.3333	2
438	2	4.4444	26	57.7778	26
444	1	2.2222	27	60.0000	30
468	1	2.2222	28	62.2222	15
492	2	4.4444	30	66.6667	31
522	2	4.4444	32	71.1111	28
558	2	4.4444	34	75.5556	10
564	1	2.2222	35	77.7778	37
576	1	2.2222	36	80.0000	17
582	1	2.2222	37	82.2222	35
630	1	2.2222	38	84.4444	34
714	1	2.2222	39	86.6667	Macroinv. grazer
768	2	4.4444	41	91.1111	Macroinv. shredders
804	1	2.2222	42	93.3333	Leuciscus idus
840	1	2.2222	43	95.5556	Botaurus stellaris
930	1	2.2222	44	97.7778	Macroinv. predator
1008	1	2.2222	45	100.0000	Lota lota

Considering only the 13-core sub web, values of density and mean degree are obviously higher than complete Ferto network, but we made a comparison with null models showing same size and density values of Ferto network. A random model network (Cohen, 1978), a cascade model network (Cohen et al., 1990) and a niche model network (Williams and Martinez, 2000) with the same size and density value of the Ferto net were generated through Foodweb3D software. Thereafter values of mean normalized density and degree of sub webs generated by k-core partition were compared with values of empirical web (table 6). The sub web generated by k-core partition of Ferto net shows higher values than simulated webs. Cohesion, in terms of links between nodes, of k-cores of real food networks seems greater than k-cores generated by different models.

Persistence of most dense k-subweb is higher than mother net, P= 0.48148.

Table 6. Mean density and degree of most dense subwebs for Ferto and simulated networks.

k-subweb	Density	Degree	Degree st dv
Ferto	0.329218	0.341880	0.0566944
Random	0.228374	0.235294	0.0364221
Cascade	0.215398	0.221925	0.0291404
Niche	0.314129	0.326211	0.0784188

Concerning dynamic food web analysis, the results are shown in Fig.8 where a 3D visualization of Lake Ferto network is depicted on the left using FoodWeb3D (Wiliams,

2003). In this image the X axis is a function of how taxa were ordered within the input data file, whereas the Y axis places nodes according to their trophic level as calculated by the program from the network structure and trophic relations between species. Therefore, primary producers and detritus compartments are at the bottom of the food web, while higher levels are occupied in order, by herbivores, predators, and parasites. Cannibalism at higher trophic level is shown by loops. Finally Z Coordinate arranges nodes in relation to greater number of links from front to back.

In Fig. 8 (right) also shows the persistent network after dynamic simulation, based on the model previously described (Martinez et al., 2005).In this case, the relative persistence of the network is calculated as the ratio between number of nodes at the beginning and at the end of the dynamical simulation and in this case is 0.42.

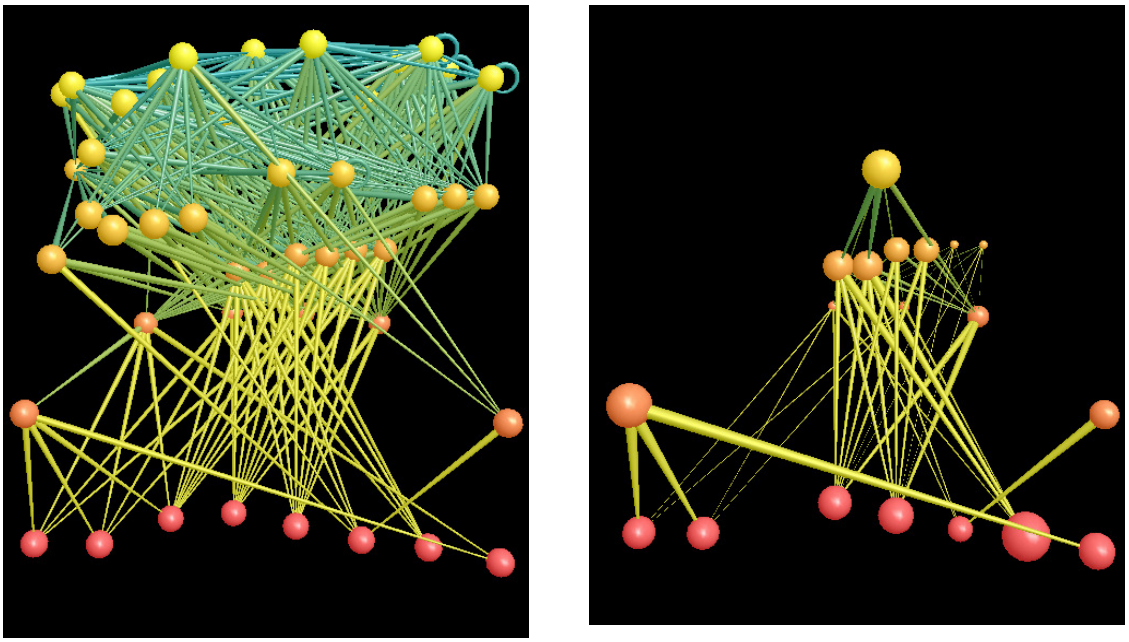

Figure 8. 3D image of lake Ferto food web obtained with the FoodWeb3D software (. Wiliams, 2003) on the left and stable net after the dynamical animation on the right.

3.2. Ria Formosa trophic network

3.2.1. General information about the site

The Ria Formosa is a sheltered large mesotidal temperate coastal lagoon located on the southern Portuguese coast (36° 58′ to 37° 03′N and 7°32′ to 8° 02′W) (J. Aníbal et al., 2006). The surface area is approximately 160 km^2, of which 48 km^2 are covered by salt marshes, 32 km^2 by a network of tidal channels and about 20 km^2 are dedicated to aquaculture ponds.

Only 14% of the surface is permanently submersed (Teixeira and Alvim, 1978) and the lagoon is covered by large beds of macroalgae and macrophytes (Loureiro et al., 2006).

Ria Formosa extends for 55 km along the coast and has a mean depth of 3.5 m and is directly connected with the ocean through several inlets (Loureiro et al., 2006).

The lagoon does not receive important freshwater input and salinity oscillates between 35.5 and 36.9 (Falcão et al., 1985).

The Ria Formosa is part of the Natura 2000 European network for nature conservation, because of its great economic and ecological value, moreover it is a Ramsar site since 1987 and it is included in the Special Bird Protection Area (European Directive 79/409/EEC). The wetland sustain a large and abundant fish community, including juvenile and commercially important fish species as seabream (*Sparus aurata*), common seabream (*Diplodus sargus*), seabass (*Dicentrarchus labrax*), sole (*Solea senegalensis*) and the eel (*Anguilla anguilla*) (Ribeiro et al., 2007); in the lagoon take place many human activities, including tourism, aquaculture, shipping, fishing, harvesting of bait, salt production and sediment extraction (Ribeiro et al., 2007). The lagoon is also an important nursery and feeding place for numerous species of shellfish and fishes. The most important shellfish species are the clam *Ruditapes decussatus* and the oyster *Crassostrea angulata* (Falcão et al, 2003).

Plant diversity and the strategic position between Europe and Africa in Ria Formosa lead to a remarkable abundance of bird fauna. Birds find in this lagoon a shelter for the winter or a resting-place. Characteristic bird species are, among others, the eurasian wigeon (*Anas Penelope*), northern shoveller (*Anas clypeata*), eurasian teal (*Anas crecca*), common pochard (*Aythya ferina*), and the great cormorants (*Phalacrocorax carbo*), avocet (*Recurvirostra avosetta*), little egret (*Egretta garzetta*), white stork (*Ciconia ciconia*), flamingos (*Phoenicopterus rubber*) and grey herons (*Ardea cinerea*) and also the rare purple swamphen (*Porphyrio porphyrio*) (Falcão et al., 2003)..

The reptile, chameleon (*Chamaeleo chamaeleon*) is a specie threaten to extinction and its distribution in Portugal is restricted to the eastern part of the Algarve (Falcão et al., 2003)..

Mammals like the otter (*Lutra lutra*), genet (*Genetta genetta*), weasel (*Martes foina*), badger (*Meles meles*) and the fox (*Vulpes vulpes*), are also part of the Ria Formosa fauna diversity (Falcão et al., 2003)..

In the last years the agricultural and urban development has lead to nutrient enrichment and a progressive reduction of water quality of the lagoon. The deterioration has been only partially contrasted by urban waste water treatment plants and improvement in lagoon water circulation (Ribeiro et al., 2007).

Trophic network compartments considered and information about species composition and diet are summarized in table 7.

Table 7. Summary of compartments, species or group of species and nodes in the Ria Formosa lagoon; databases and references relative to species composition and diet are reported.

Reference species composition	Compartments	Species or groups	Nodes	References diet
Ribeiro, 2006; Oliveira, 2007	Fish	81	21	Oliveira, et al., 2007; Ribeiro et al., 2006; http://www.fishbase.org/ (Jellyman,1989)
CORINE and Natura 2000	Amphibians	4	3	Schleich, 1996; Smith, 1969; http://amphibiaweb.org/
CORINE and Natura 2000	Mammals	7	7	Moleón and Gil-Sánchez, 2003; Myers, et al., 2006; Soriguer and Amat, 1988; http://www.abdn.ac.uk/mammal/index
CORINE and Natura 2000	Reptiles	10	7	Castilla et al., 1991;Díaz and Carrascal, 1993; Lopez & Martin, 2001; Saenz et al., 1996; http://nlbif.eti.uva.nl/bis/turtles; http://www.batraciens-reptiles.com/; www.mediterranea.org/cae;
CORINE and Natura 2000	Birds	123	25	Ankney & Afteon, 1988; Battern, 1990; Bottonet al., 1994; Burton & Burton, 1970; Castro & Myers, 1993; Cogswell, 1977; Cocker M. & R. Mabey, 2005; Dunn & Agro, 1995; Gooders, 1982; Holden & Sharrock, 2002; Kirschbaum & Watkins, 2000; Leo, 2006; Lack, 1986; Moon, G., 1994; Mullarney et al., 1999; Palmer, 1976; Peterson, 1961; Piatt and Nettleship, 1985; Senner et al., 1989; Sinclair et al., 2002; Skaggs et al. 1988; Taylor, B. and V. Perlo, 1998; Terres, 1980; Tsachalidis & Goutner, 2002; http://animaldiversity.ummz.umich.edu/site/index.html; http://aves.ccg.pt/; http://www.arkive.org/; Tague, 2000; http://www.hawk-conservancy.org; http://www.iucnredlist.org/; http://www.natureserve.org/; http://www.oiseaux.net/oiseaux; http://www.rspb.org.uk; http://www.specolalive.it;
Aníbal et al., 2007	Macroinvertebrates	47	15	Aníbal et al., 2007; Buck,et al., 2003; Cannicci, 2002; Christie et al., 2007; Heckscher et al., 1996; Hily et al., 2004; Kennish, R. 1996; Kofoed, 1975; Kohn & Gosselck, 1989; Malaquias & Sprung, 2005; Martins et al., 1997; Vetter, 1996; Woods,1993; Zupo, 2001; http://hbs.bishopmuseum.org/aocat/tipulidae.html; http://www.arkive.org/;
Gamito and Erzini, 2005	Meso-Macrozooplankton	3	1	Gamito and Erzini, 2005
Gamito and Erzini, 2006	Micro zooplankton	1	1	Gamito and Erzini, 2006
	Bacteria	1	1	
	Fungi	1	1	
	Phytoplankton	1	1	
	Benthic Algae	1	1	
	Epiphites	1	1	
CORINE and Natura 2000	Plants	20	1	
Aníbal et al., 2007	Macroalgae	2	1	
Aníbal et al., 2007	Seagrasses	1	1	
	Benthic detritus	1	1	
	Plankton detritus	1	1	

3.2.2. Network analysis

A visualization of Ria Formosa food web is shown in figure 9, names of species or group of species are missing to avoid superimposition, and are instead listed in table 8, as previously primary producers and detritus are on the top and predators on the bottom. Ria Formosa network appear more complex that lake Ferto net, size of the net is 90, the total number of ties is 1253 and 6 loops, density is 0.1526, therefore about 15% of possible links are present in the net.

The distribution of degree is homogeneous (table 9), species with the higher degree are macroinveterbrates, crustaceans and omnivorous birds. Mean degree of the network is 27.84 (standard deviation 13.11), the normalized mean degree is 0.1564295 (standard deviation 0.073). In Ria Formosa network we identified three types of cores: k input cores, output cores,

calculated taking into account respectively incoming and outgoing lines, and cores that ignore the direction of lines. We found three input and three output cores (figure 10). Rank distribution is in general in agreement with trophic level; in particular fish, some mammals and bird classes belong to higher input core rank, whereas macroinvetebrates belong to higher output core rank.

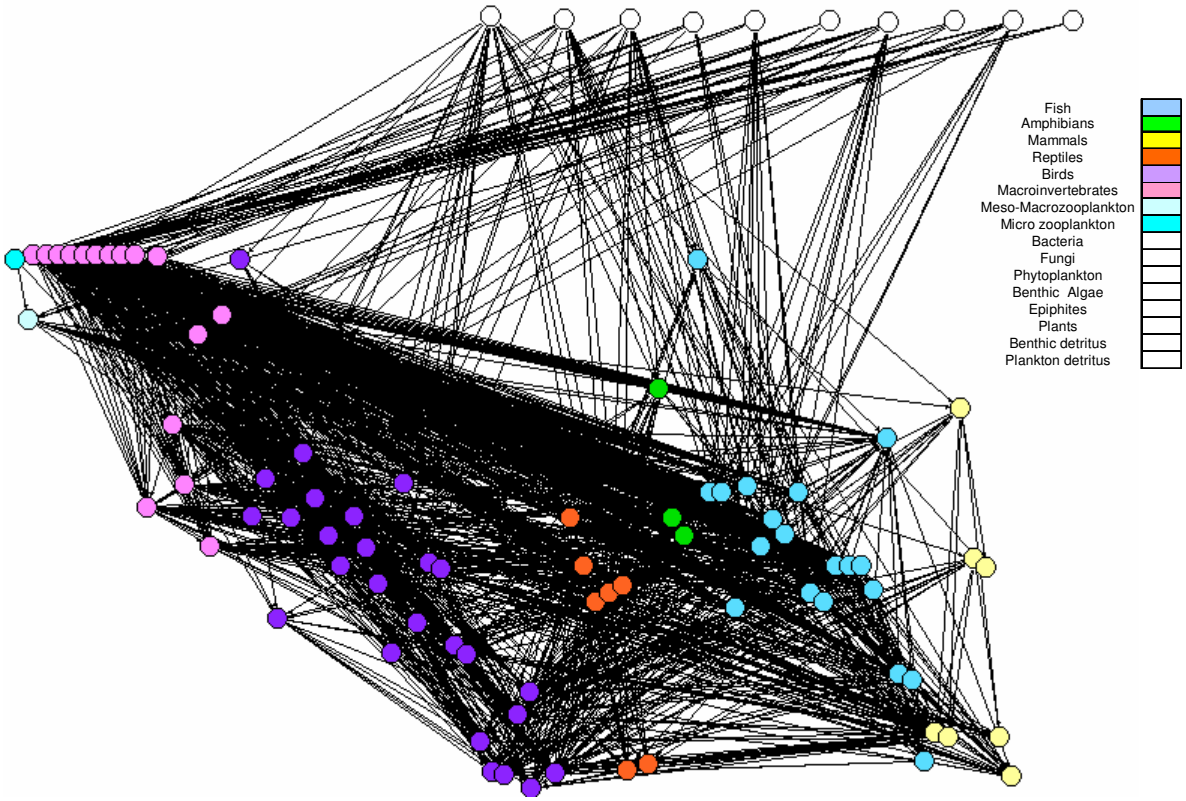

Figure 9. Ria Formosa trophic network, vertices are ordered according to their trophic level, colours indicate different compartments

Table 8. List of species and compartments in Ria Formosa food web.

Lutra lutra Felis silvestris Mustela putorius Suncus etruscus Microtus cabrerae Herpestes ichneumon Genetta genetta	Mammals
Belone belone Conger conger Anguilla anguilla Sparus auratus Torpedo marmorata Dentex dentex Dicentrarchus punctatusPagellus erythrinusSolea senegalensis Lithognathus mormyrusTrachinus draco Syngnathus acus Halobatrachus didactylusBothus podas Dentex marocanus Nerophis ophidion Syngnathus abaster Pagellus acarne Syngnathus typhle Echiichthys vipera Arnoglossus laterna Arnoglossus thori Symphodus rostratusScorpaena notata Serranus hepatus Raja undulate Scophthalmus rhombus Alosa alosa Labrus bergyltaLabrus merula Pegusa lascaris Microchirus azevia Diplodus bellottii Hippocampus guttulatus Callionymus risso Gobius couchi Gobius cruentatus Gobius niger Gobius paganellus Pomatoschistus microps Pomatoschistus minutus Pomatoschistus pictus Diplecogaster bimaculata Symphodus roissali Callionymus maculatusAtherina sp.Symphodus cinereus Labridae Ctenolabrus rupestris Scorpaena porcus Scophthalmus maximus Trigla lucerna Diplodus vulgarisSerranus cabrilla Diplodus annularisSpondyliosoma cantharusDiplodus puntazzoDiplodus cervinus Symphodus melops Rutilus lemmingiiParablennius gattorugine Symphodus ocellatus Salaria pavoParablennius pilicornisEngraulis encrasicholusSardina pilchardusDiplodus sargus Rutilus alburnoides Dicentrarchus labraxChelon labrosusMugil cephalusLiza ramadaHippocampus hippocampusNerophis lumbriciformesLiza auratusLiza saliens Mullus surmuletus Mullus barbatusSarpa salpaMicrochirus boscanion Monochirus hispidus Symphodus bailloni Synaptura lusitanica Martes foina Meles meles Vulpes vulpes	Fish
Bufo calamita Hyla meridionalis Pelobates cultripes Bufo bufo	Amphibians
Elaphe scalaris Chamaeleo chamaeleon Emys orbicularis Mauremys leprosa Lacerta lepida Acanthodactylus erythrurus Hemidactylus turcicus Psammodromus algirus Psammodromus hispanicus Chalcides bedriagai	Reptiles
Pandion haliaetusCircus aeruginosusPhalacrocorax carboSterna hirundoSterna sandvicensisMergus serratorAlca torda Alcedo atthis Ardea cinerea Ardea purpurea Ardeola ralloides Nycticorax nycticoraxFalco peregrinusCircus cyaneusHieraaetus pennatusMilvus migrans Circus pygargusBurhinus oedicnemus Ciconia ciconia Clamator glandariusTringa nebulariaPlatalea leucorodiaTringa totanus Ixobrychus minutusSterna caspiaSterna albifrons Egretta garzettaChlidonias niger Calidris canutus Larus minutus Larus fuscusNetta rufina Porphyrio porphyrioLarus ridibundusAnas clypeata Cyanopica cyanus Aythya fuligula Charadrius alexandrinus Numenius arquataPluvialis apricariaErithacus rubeculaGallinago gallinagoAnas crecca Anas querquedula Anthus pratensisLimosa lapponica Acrocephalus schoenobaenus Pluvialis squatarolaPorzana pusilla Tetrax tetraxSylvia borinPhoenicurus	Birds

ochrurosPhoenicopterus ruber Haematopus ostralegusNumenius phaeopusPodiceps nigricollisPhilomachus pugnax Charadrius hiaticula Recurvirostra avosetta Vanellus vanellus Calidris ferruginea Larus melanocephalus Himantopus himantopus Tadorna tadorna Tringa erythropusCalidris alpina schinzii Tringa ochropusTringa glareolaMotacilla cinereaCalidris alba Motacilla flavaLimosa limosa Calandrella brachydactyla Sylvia cantillansGalerida theklae Luscinia svecicaPhylloscopus trochilusLullula arboreaCercotrichas galactotesLuscinia megarhynchosAnthus campestrisFicedula hypoleuca Sylvia communisOenanthe oenantheSylvia conspicillataSylvia undataTurdus iliacus Streptopelia turtur Porzana porzana Melanocorypha calandra Caprimulgus ruficollis Delichon urbicaGlareola pratincolaHippolais polyglottaHippolais pallida Hirundo rusticaCuculus canorusAnthus trivialis Acrocephalus scirpaceusAnthus spinoletta Apus apus Turdus philomelos Riparia ripariaApus pallidus Locustella luscinioidesLocustella naeviaMuscicapa striataOenanthe hispanicaPhylloscopus bonelliSaxicola rubetraScolopax rusticola Phoenicurus phoenicurus Regulus ignicapillusMerops apiasterAcrocephalus arundinaceus Calidris alpina Calidris minuta Anas penelope	
	Terrestrial Macroinvertebrates
Gnathiidae Crangon crangon Carcinus maenas Pachygrapsus marmoratus Palaemon elegansPalaemon serratus Hippolyte inermis Crabs sp.Rissoa membranaceaTurritellidaeBittium reticulatum Rissoa membranacea Gibbula varia Gibbula umbilicalis Cerithium vulgatum Amyclina corniculum Haminoea naviculaHaminoea orbygnianaMicrodeutopus sp. (larvae) Tipulidae Ruditapes decussatusHydrobia Hydrobia ulvae Hydrobia ventrosaPolychaetesGammarus sp.Sphaeroma spp. Idotea chelipes Chironomidae Tanais dulongii Zenobiana sp.Cyathura carinata Melita palmata Holothuria sp. Nassarius pfeifferi Nebalia sp. Palaemonetes varians Hippolyte varians Hippolyte longirostris Thoralus cranchii Elasmopus rapazShrimps sp.	Macroinvertebrates
	Macro-mesozooplankton
	Microzoo plankton
Tuberaria major Thymus carnosusThymus cephalotosArmeria velutinaLinaria algarvianaLimonium lanceolatum Melilotus segetalis ssp. fallax Riella helicophylla Campanula primulifolia Loeflingia tavaresiana Thymus carnosus Cistanche phelypaea Limonium diffusum Armeria macrophylla Armeria pinifolia Linaria lamarckii Scilla odorata Bellevalia hackelii Limonium lanceolatum Malcolmia lacera ssp. gracilima Thymus lotocephalus	Plants
Enteromorpha Ulva	Macroalgae
Zostera noltii	Seagrass
	Phytoplankton
	Benthic Algae
	Epiphites
	Bacteria
	Fungi
	Benthic detritus
	Plankton detritus

Table 9. Frequency distribution of degree in the Ria Formosa net.

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
3	1	1.1111	1	1.1111	Mustela putorius
4	1	1.1111	2	2.2222	Plankton detritus
5	3	3.3333	5	5.5556	Microzoo plankton
8	1	1.1111	6	6.6667	Phytoplankton
11	4	4.4444	10	11.1111	Anas penelope
12	2	2.2222	12	13.3333	Birds insectivorous
13	4	4.4444	16	17.7778	Birds insectivorous/graniv
14	1	1.1111	17	18.8889	Suncus etruscus
15	3	3.3333	20	22.2222	Acrocephalus arundinaceus
16	1	1.1111	21	23.3333	Insectiv.reptiles
17	3	3.3333	24	26.6667	Chamaeleo chamaeleon
18	3	3.3333	27	30.0000	Birds pred 1
19	2	2.2222	29	32.2222	Calidris alpina
20	2	2.2222	31	34.4444	Omniv.reptiles
22	2	2.2222	33	36.6667	Macro-mesozooplankton
23	5	5.5556	38	42.2222	Birds invertivorus 1
24	3	3.3333	41	45.5556	Calidris minuta
26	3	3.3333	44	48.8889	Birds invertivorus 2
27	2	2.2222	46	51.1111	Bufo calamita
28	1	1.1111	47	52.2222	Birds pred 2
29	1	1.1111	48	53.3333	Hemidactylus turcicus
30	3	3.3333	51	56.6667	Pycnogonida
31	3	3.3333	54	60.0000	Fish omniv-detrit 2
32	1	1.1111	55	61.1111	Circus aeruginosus
33	1	1.1111	56	62.2222	Genetta genetta
35	3	3.3333	59	65.5556	Piscivore birds
38	3	3.3333	62	68.8889	Microdeutopus sp.
39	4	4.4444	66	73.3333	Dicentrarchus labrax
40	6	6.6667	72	80.0000	Macroinvertebrates scavengers
41	5	5.5556	77	85.5556	Crustaceans scraper/shredder
42	3	3.3333	80	88.8889	Rissoa membranacea

43	3	3.3333	83	92.2222	Ruditapes decussatus
45	1	1.1111	84	93.3333	Crustaceans ominv/pred
48	2	2.2222	86	95.5556	Gastropods deposit or filter feeding
52	1	1.1111	87	96.6667	Birds pred 5
53	1	1.1111	88	97.7778	Crabs sp.
54	1	1.1111	89	98.8889	Macroinvertebrates collectors
55	1	1.1111	90	100.0000	Pandion haliaetus

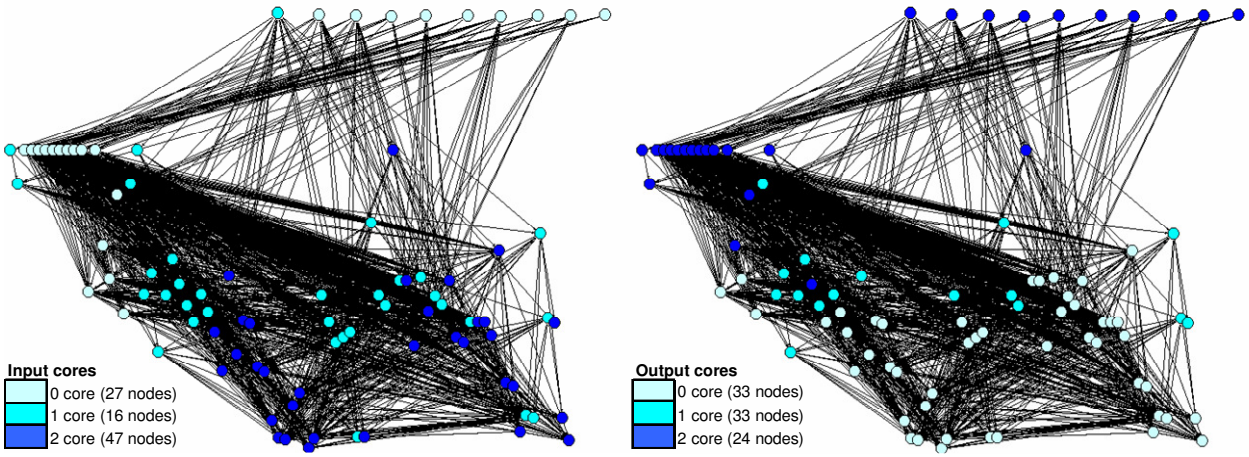

Figure 10. Input and output cores in the Ria Formosa network, colours indicate vertices belonging the different cores.

Partition in k-cores (figure11 and table 10) pointed out again the presence of one big core, with 34 vertices linked with at least 21 other nodes within the core. The main core contains macroinvertebrates, fish and only one reptile (*Mauremys leprosa*) (figure 12). Several smaller cores have been detected inside the Ria Formosa network, which show an overall organization in cohesive subgroup, only two nodes (phytoplankton and *Mustela putorius*) are not included in any subwebs. Again primary producers belong to subwebs with lower density.

Table 10. Frequency distribution of k-cores in the Ria Formosa network

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
3	1	1.1111	1	1.1111	Mustela putorius
4	2	2.2222	3	3.3333	Microzoo plankton
5	2	2.2222	5	5.5556	Epiphites
7	1	1.1111	6	6.6667	Phytoplankton
11	4	4.4444	10	11.1111	Anas penelope
12	5	5.5556	15	16.6667	Birds insectivorous
13	4	4.4444	19	21.1111	Elaphe scalaris
14	3	3.3333	22	24.4444	Acrocephalus arundinaceus
15	3	3.3333	25	27.7778	Circus cyaneus
16	9	10.0000	34	37.7778	Calidris alpina
17	3	3.3333	37	41.1111	Birds pred 1
18	8	8.8889	45	50.0000	Macro-mesozooplankton
19	2	2.2222	47	52.2222	Birds invertivorus 2
20	9	10.0000	56	62.2222	larvae Tipulidae
21	34	37.7778	90	100.0000	Macroinvertebrates scavengers

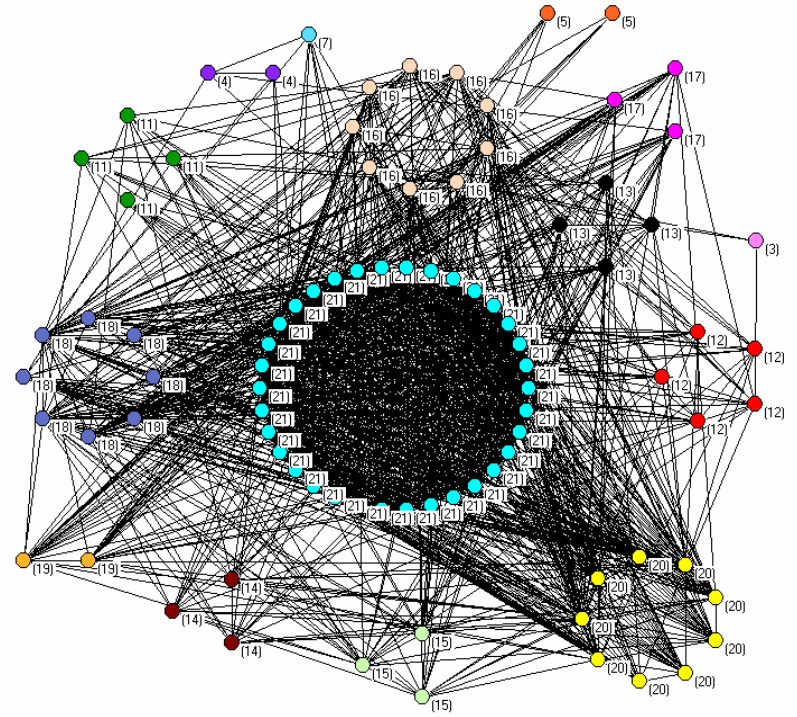

Figure 11. K-cores partition in Ria Formosa network, colours indicate the different k cores and partition class number are used to mark vertices.

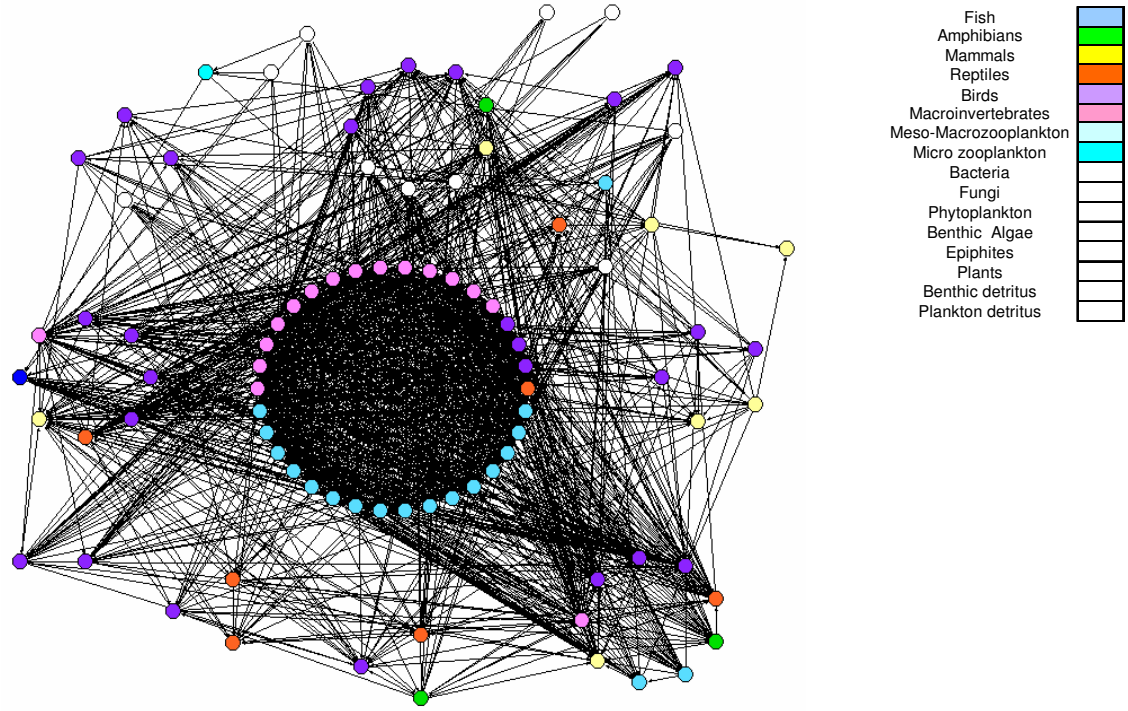

Figure 12. K-cores partition in Ria Formosa network, colours indicate the different compartments.

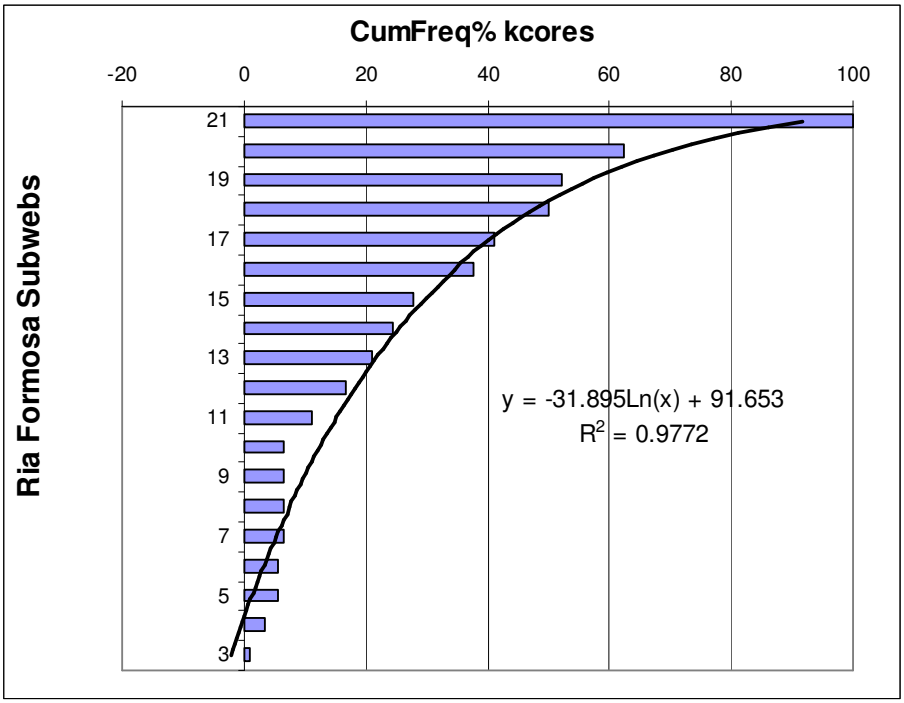

Figure 13. K-subwebs cumulative frequency distribution in Ria Formosa net.

Cumulative frequency distribution of k-cores in Ria Formosa network (Fig. 13) follows, with a very good approximation, as in the case of Ferto lake a logarithmic law.

One strong component (Fig.e 14) has been detected inside the main core of Ria Formosa web; only three vertices, in particular crustaceans predators classes, belong to the component, indicating cannibalism inside similar trophic compartments.

In figure 14 nodes of the main core have been drawn using visualization commands in a way to minimize the variation in the length of ties, and manually adjusted to circles approximation layout. Distance between nodes expresses the strength of connection.

All vertices are interconnected through weak paths (unidirectional ties). Many triads can be identified inside the net (table 11). Higher class number are assigned to custaceans and omivourus fish compartments on of Ria Formosa network

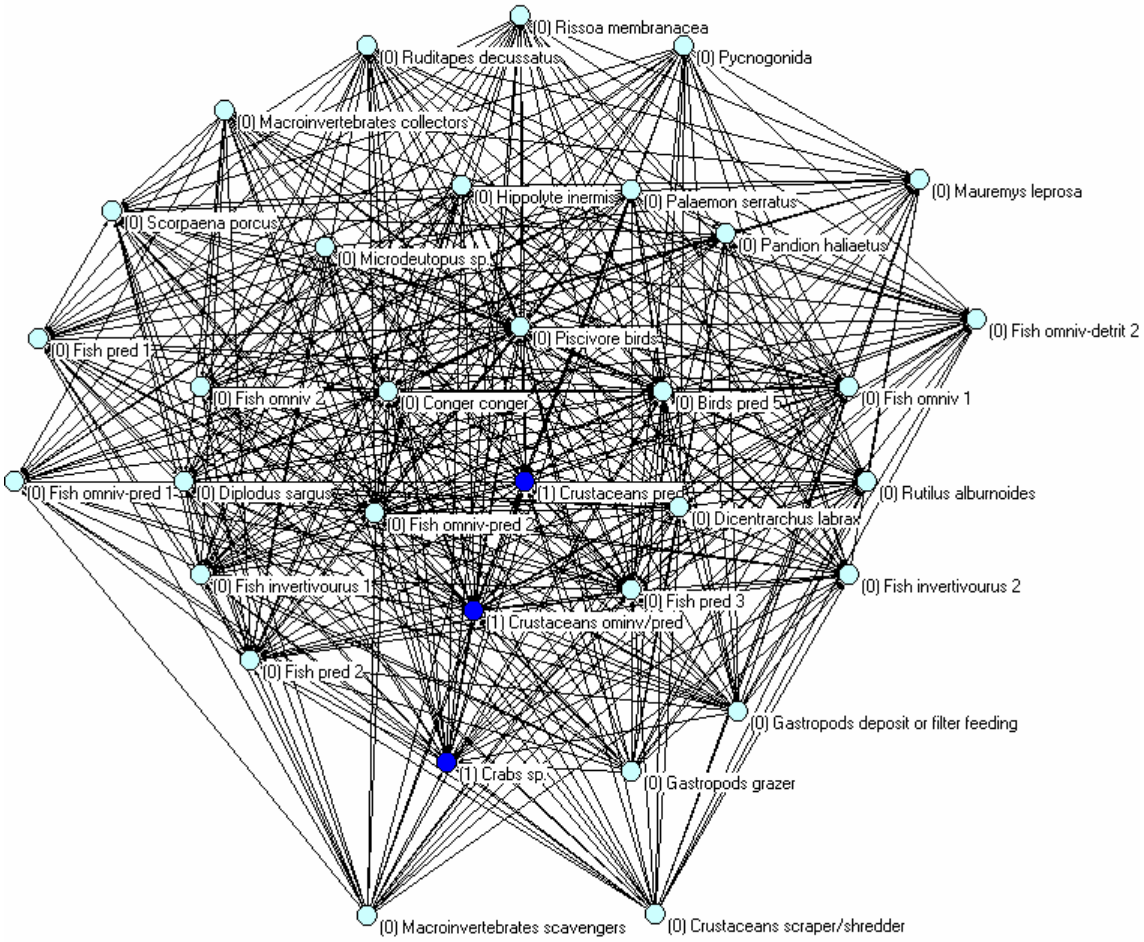

Figure 14. K-cores partition in Ria Formosa network, colour blue indicates a strong component. Labels indicate partition class numbers and species or compartment.

Table 11. Frequency distribution of triads in the lake Ferto network.

Class	Freq	Freq%	CumFreq	CumFreq%	Representative
696	1	2.9412	1	2.9412	Mauremys leprosa
858	1	2.9412	2	5.8824	Fish omniv-detrit 2
876	1	2.9412	3	8.8235	Pandion haliaetus
978	2	5.8824	5	14.7059	Fish omniv-pred 1
1020	6	17.6471	11	32.3529	Macroinvertebrates scavengers
1068	1	2.9412	12	35.2941	Fish omniv 2
1122	3	8.8235	15	44.1176	Ruditapes decussatus
1152	1	2.9412	16	47.0588	Palaemon serratus
1200	2	5.8824	18	52.9412	Fish omniv-detrit 1
1380	1	2.9412	19	55.8824	Gastropods deposit or filter feeding
1392	1	2.9412	20	58.8235	Fish pred 1
1476	2	5.8824	22	64.7059	Fish omniv 1
1530	1	2.9412	23	67.6471	Scorpaena porcus
1794	1	2.9412	24	70.5882	Diplodus sargus
1980	1	2.9412	25	73.5294	Dicentrarchus labrax
2004	3	8.8235	28	82.3529	Birds pred 5
2160	1	2.9412	29	85.2941	Crabs sp.
2286	2	5.8824	31	91.1765	Crustaceans ominv/pred
2292	3	8.8235	34	100.0000	Fish omniv-pred 2

As for the Ferto net, random, cascade and niche model with same size and density of Ria Formosa food web were generated and for each simulated network the main k-core was extracted. Measure of mean density and normalized degree of higher k-cores, for empirical and simulated networks are shown in table 12. In agreement with results obtained for Ferto lake, density and degree of k-core extracted from Ria Formosa network are higher than the others; the model that reproduce more accurately the empirical distribution of links between species is the niche model. In the random and cascade model the main core account for the 95.5% of all nodes, whereas in the niche model, for the 61.1% and in the Ria Formosa only for the 37.7%.

Table 12. Mean density and degree of most dense subwebs for Ferto and simulated networks.

k-subweb	Density	Degree	Degree st dv
Ria Formosa	0.3814879	0.3930481	0.0665472
Random	0.1537317	0.1555404	0.0235397
Cascade	0.1594105	0.1612859	0.0230886
Niche	0.2476033	0.2521886	0.0660173

A 3D visualization of Ria Formosa network obtained with the software FoodWeb3D (R.J. Wiliams, 2003) before and after the dynamical simulation is shown in figure 8.

In case of Ria Formosa network, the greater complexity decrease the overall food web stability (persistence 0.26). The debate on the link between complexity and stability of the trophic network is a central theme in ecology (Garcia Domingo and Saldaña, *in press*). The role of connectance, weak links and adaptive predation seems still unclear and results of different studies are conflicting or show methodological lacks, using models that are not able to reproduce empirical trophic networks (Kondoh, 2003; Brose et al., 2003;)

Relative persistence of the k-core sub network is 0.5, again higher than mother web.

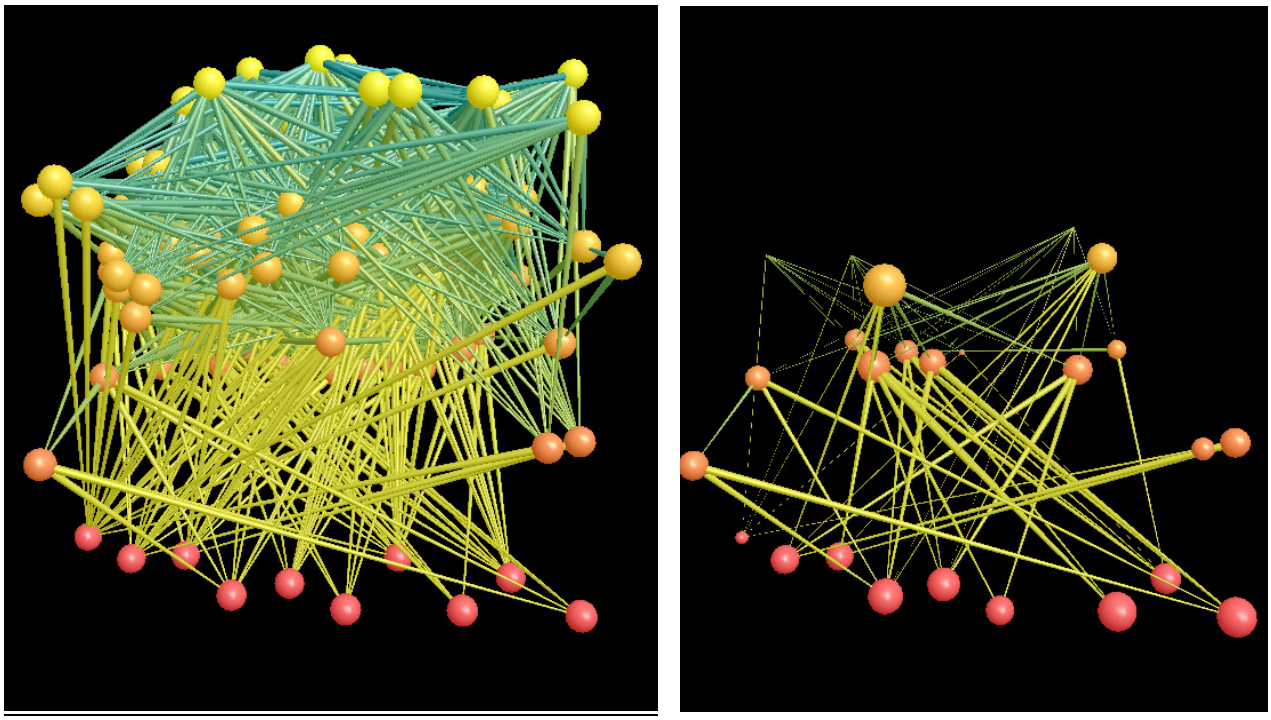

Figure 15. 3D image of Ria Formosa food web obtained with the FoodWeb3D software (R.J. Wiliams, 2003) on the left and stable net after the dynamical animation on the right.

4. Preliminary Conclusions

In this work we have defined and analyzed the network structure, properties and composition of cohesive sub webs in two food web networks at two selected European sites: Ferto lake in Hungary and Ria Formosa lagoon in Portugal, which are located in the Pannonian and Mediterranean zones, respectively. The main object of this work was to test and to apply a coherent methodology for the definition and analysis of trophic networks in typical European ecosystems.

Persistence and cohesion of the two networks have been determined and studied. Moreover the biodiversity in terms of number of species have been measured.

Several preliminary conclusions can be drawn on a basis of results obtained from application of network analysis indices and dynamical simulation.

Two biodiversity indices, Shannon-Weiner and Simpson's, have been applied to the networks analyzed. The Shannon-Weiner and the Simpson's indices for Ferto lake are 1.76863 and 0.22744, whereas for Ria Formosa lagoon are 1.53347 and 0.277488, respectively Surprisingly, the Shannon–Weiner index assigns the highest value to the Ferto lake foodweb.

This result can be due to an unbalanced distribution of species between compartments in the Ria Formosa lagoon, in fact the birds compartment account for 27.2 % of all network, whereas in the Ferto lake distribution of abundances is more homogeneous.

In terms of stability the lake Ferto network (persistence 0.42) seems more stable than Ria Formosa (persistence 0.26), but if we consider the stability of the main k-core, we obtain opposite results (0.48 and 0.50, respectively). However, the equation applied for the definition of stability is very sensitive to the size of the network and therefore more reliable results may be drawn from the application to the main k-cores.

Taking into account distribution of species in the k-core partition, the general structure of Ria Formosa network appears more complex than Ferto lake. In both networks a main core containing species taxonomically different is present, but in the Ria Formosa network (37.7%) the proportion of species inside the core is lower than Ferto lake (60%), this can be an indication that the dimension of the main core is not related to size of the network in real ecosystems. This hypothesis is confirmed by results obtained from k-core partition of simulated networks.

In both studied networks the cohesion (measured in terms of mean density and degree) of k-cores is greater than k-cores extracted from simulated networks generated by different models, this may indicate a complex and not arbitrary structure of empirical networks, not easily reproducible by models.

The approach proposed here appear to be able of defining the main proprieties of trophic networks examined. The extension to other European ecosystems is needed for having a clearer and complete picture and to use data collected to simulation of different scenarios, afterwards the effects on network structure and ecosystem biodiversity as a function of different European environmental policies could be assessed.

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Abstract
In this work we have defined and analyzed the network structure, properties and composition of cohesive sub webs in two food web networks at two selected European sites: Ferto lake in Hungary and Ria Formosa lagoon in Portugal, respectively. The main objective of this work was to test and to apply a coherent methodology for the definition and analysis of trophic networks in typical European ecosystems. Persistence and cohesion of the two networks have been determined and studied. Moreover the biodiversity in terms of number of species have been measured. Several preliminary conclusions can be drawn on a basis of results obtained from application of network analysis indices and dynamical simulation. In terms of ecosystem stability the lake Ferto network (persistence 0.42) seems more stable than Ria Formosa (persistence 0.26), but if we consider the stability of the main k-core, we obtain opposite results (0.48 and 0.50 respectively).
Taking into account the distribution of species in the k-core partition, the general structure of Ria Formosa network appears more complex than Ferto lake. In both networks a main core containing species taxonomically different is present, but in the Ria Formosa network (37.7%) the proportion of species inside the core is lower than in Ferto lake (60%), this can be an indication that the dimension of the main core is not related to size of the network in real ecosystems. This hypothesis is confirmed by results obtained from k-core partition of simulated networks. In both studied networks the cohesion (measured in terms of mean density and degree) of k-cores is greater than k-cores extracted from simulated networks generated by different models, this may indicate a complex and not arbitrary structure of ecological networks, not easily reproducible by models. In general the approach used appears to be able of defining the main proprieties of the trophic networks examined. The extension to other European ecosystems is needed for having a clearer and complete picture and to use data collected to simulation of different scenarios, afterwards the effects on network structure and ecosystem biodiversity as a function of different European environmental policies could be assessed.

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